

HS prok gamma Differential expression HvA_names

All records per page

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ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_369918_9_AAA_domain		-8.10	3.27e-05	0.012700	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_369918_9_AAA_domain.p...
k141_179467_12_Part_of_a_membrane_complex_involved		-7.81	1.59e-04	0.022500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_179467_12_Part_of_a_m...
k141_173944_24_Bacterial_Fe_2+_trafficking		-7.51	7.08e-05	0.018400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_173944_24_Bacterial_Fe...
k141_294638_3_The_glycine_cleavage_system_catalyze		-7.46	2.58e-04	0.026000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_294638_3_The_glycine_cl...
k141_121273_10_Sulfatase-modifying_factor_enzyme_1		-7.42	6.57e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_121273_10_Sulfatase-mo...
k141_15476_7_Belongs_to_the_universal_stress_prote		-7.42	1.58e-04	0.022500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_7_Belongs_to_the...
k141_302855_3_Putative_restriction_endonuclease		-7.16	3.92e-04	0.029100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_302855_3_Putative_restri...
k141_171717_3_Belongs_to_the_membrane_fusion_prote		-7.05	1.01e-03	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_171717_3_Belongs_to_th...
k141_400150_3_Citrate_transporter		-6.93	1.12e-03	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_400150_3_Citrate_transp...
k141_370813_25_Protein_of_unknown_function__DUF288		-6.92	1.12e-03	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_370813_25_Protein_of_un...
k141_491901_9_Isocitrate_lyase		-6.91	2.40e-07	0.000338	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_491901_9_Isocitrate_lyas...
k141_26457_23_Urease_gamma_subunit		-6.87	2.65e-03	0.041000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_26457_23_Urease_gam...
k141_143273_4_ATPase_family_associated_with_variou		-6.77	6.63e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143273_4_ATPase_family...
k141_480101_6_imidazoleglycerol-phosphate_dehydrat		-6.77	1.04e-03	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_6_imidazoleglyce...
k141_384551_3_-		-6.74	1.08e-03	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_384551_3_..pdf)
k141_145339_6_Protein_of_unknown_function__DUF2892		-6.72	7.82e-05	0.018400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_145339_6_Protein_of_unk...
k141_151495_3_OsmC-like_protein		-6.67	1.25e-03	0.033300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_151495_3_OsmC-like_pro...
k141_55232_16_Belongs_to_the_bacterial_ribosomal_p		-6.60	1.68e-03	0.036300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_16_Belongs_to_th...
k141_114613_1_Tetratricopeptide_repeat		-6.59	7.69e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_114613_1_Tetratricopeptid...
k141_239940_8_Domain_of_unknown_function__DUF3541_		-6.58	1.38e-03	0.034900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_239940_8_Domain_of_un...
k141_402410_4_Putative_restriction_endonuclease		-6.58	1.48e-03	0.034900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_402410_4_Putative_restri...
k141_491901_10_Isocitrate		-6.52	2.50e-03	0.041000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_491901_10_Isocitrate.pdf)
k141_189812_1_HflK_and_HflK_could_regulate_a_prote		-6.51	1.22e-03	0.033000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_1_HflK_and_HflK...
k141_447245_37_Metallo-beta-lactamase_superfamily		-6.50	1.91e-03	0.037000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447245_37_Metallo-beta-l...
k141_441355_17_Activates_fatty_acids_by_binding_to		-6.49	1.08e-03	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_441355_17_Activates_fatt...
k141_92968_30_Fe-S_cluster		-6.48	6.96e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_30_Fe-S_cluster.pdf)
k141_435897_2_AAA_domain		-6.43	7.13e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_435897_2_AAA_domain.p...
k141_480234_56_PFAM_Glutathione_S-transferase		-6.42	2.08e-03	0.038100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_56_PFAM_Glutat...
k141_55541_33_PFAM_Prephenate_dehydratase		-6.42	5.06e-03	0.055300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_33_PFAM_Prephe...
k141_196338_28_chlorophyll_binding		-6.40	4.37e-03	0.052700	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_196338_28_chlorophyll_bi...
k141_355308_3_Belongs_to_the_AlaDH_PNT_family		-6.40	1.58e-03	0.036300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_355308_3_Belongs_to_th...
k141_411766_1_5'-nucleotidase__C-terminal_domain		-6.40	6.57e-03	0.056800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_411766_1_5'-nucleotidase...
k141_171717_5_MacB-like_periplasmic_core_domain		-6.39	1.73e-03	0.036300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_171717_5_MacB-like_peri...
k141_445026_12_Belongs_to_the_glycosyl_hydrolase_5		-6.37	2.05e-03	0.038100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_445026_12_Belongs_to_t...
k141_318301_56_Bacterial_protein_of_unknown_funcit		-6.36	1.88e-03	0.037000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_56_Bacterial_prot...

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_116678_42_CNP1-like_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116678_42_CNP1-like_fa...	-6.33	2.50e-03	0.041000
k141_183936_6_Belongs_to_the_5-formyltetrahydrofol		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183936_6_Belongs_to_th...	-6.31	4.57e-03	0.054600
k141_55232_22_Phosphate-selective_porin_O_and_P		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_22_Phosphate-se...	-6.30	1.49e-03	0.034900
k141_55541_41_Catalyzes_the_decarboxylation_of_oro		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_41_Catalyzes_the...	-6.29	5.04e-03	0.055300
k141_321119_1_Belongs_to_the_5'-nucleotidase_famil		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_1_Belongs_to_th...	-6.27	3.73e-03	0.049100
k141_183936_4_TIGRFAM_TIGR02449_family_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183936_4_TIGRFAM_TIG...	-6.25	5.48e-03	0.055300
k141_347826_2_Belongs_to_the_SfsA_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_347826_2_Belongs_to_th...	-6.25	8.93e-03	0.064300
k141_486291_3_Fad_linked_oxidase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_3_Fad_linked_oxi...	-6.22	1.70e-03	0.036300
k141_370813_13_Catalyzes_the_synthesis_of_5_6-dihy		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_370813_13_Catalyzes_th...	-6.18	5.24e-03	0.055300
k141_189812_15_Responsible_for_synthesis_of_pseudo		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_15_Responsible_...	-6.15	6.85e-03	0.056800
k141_335000_11_The_RuvA-RuvB_complex_in_the_presen		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_335000_11_The_RuvA-R...	-6.13	4.18e-03	0.052600
k141_55541_10_Dynamin_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_10_Dynamin_famil...	-6.13	2.67e-03	0.041000
k141_207353_8_carbamoyl_transferase__NodU_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_207353_8_carbamoyl_tra...	-6.11	8.84e-03	0.064200
k141_92968_2_Cysteine-rich_CPXCG		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_2_Cysteine-rich_C...	-6.10	5.65e-03	0.055300
k141_105059_49_Cleaves_type-4_fimbrial_leader_sequ		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_49_Cleaves_type...	-6.08	7.81e-03	0.059600
k141_15043_26_pfam_abc		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15043_26_pfam_abc.pdf)	-6.08	6.55e-03	0.056800
k141_155751_11_Domain_of_unknown_function__DUF4124		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_155751_11_Domain_of_u...	-6.02	7.11e-03	0.056800
k141_183573_4_SMART_cyclic_nucleotide-binding		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183573_4_SMART_cyclic...	-6.02	5.35e-03	0.055300
k141_400150_9_Chloride_channel		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_400150_9_Chloride_chan...	-5.98	7.05e-03	0.056800
k141_55541_23_Involved_in_peptide_bond_synthesis__		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_23_Involved_in_pe...	-5.98	6.84e-03	0.056800
k141_411118_44_PFAM_peptidase_S49		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_411118_44_PFAM_peptid...	-5.97	5.11e-03	0.055300
k141_55232_1_Belongs_to_the_WrbA_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_1_Belongs_to_the...	-5.97	7.26e-03	0.057200
k141_181027_9_Specifically_methylates_the_N7_posit		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_181027_9_Specifically_m...	-5.96	5.34e-03	0.055300
k141_480234_12_Catalyzes_the_conversion_of_N5-carb		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_12_Catalyzes_th...	-5.96	1.27e-02	0.072900
k141_198809_11_it_binds_specifically_double-strand		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198809_11_it_binds_spec...	-5.92	5.57e-03	0.055300
k141_181756_13_Phosphoglycerate_mutase_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_181756_13_Phosphoglyc...	-5.91	6.42e-03	0.056800
k141_390169_29_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_29_-pdf)	-5.90	1.29e-02	0.073500
k141_105059_14_Catalyzes_the_condensation_of_panto		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_14_Catalyzes_th...	-5.89	1.09e-02	0.068900
k141_105059_7_Domain_of_unknown_function__DUF2760_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_7_Domain_of_un...	-5.88	7.07e-03	0.056800
k141_480101_13_Protein_of_unknown_function__DUF255		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_13_Protein_of_un...	-5.88	1.07e-02	0.068900
k141_26457_18_TrkA-C_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_26457_18_TrkA-C_domai...	-5.83	1.14e-02	0.070300
k141_335000_12_The_RuvA-RuvB_complex_in_the_presen		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_335000_12_The_RuvA-R...	-5.83	1.09e-02	0.068900
k141_390169_33_PFAM_lipolytic_protein_G-D-S-L_fami		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_33_PFAM_lipolyti...	-5.83	9.82e-03	0.067300
k141_445525_9_Peptidase_S24-like		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_445525_9_Peptidase_S24...	-5.83	1.14e-02	0.070300
k141_480234_35_Sigma_54_modulation_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_35_Sigma_54_m...	-5.82	1.23e-02	0.072100
k141_92968_32_Part_of_a_membrane_complex_involved__		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_32_Part_of_a_me...	-5.82	4.31e-03	0.052700
k141_91609_13_PFAM_Toluene_tolerance		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_91609_13_PFAM_Toluene...	-5.78	1.48e-02	0.076200

ID	Image	logFC	From	From	From
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			p-Value	Adjusted p-Value	
k141_331758_16_peptidase_M48_Ste24p		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_331758_16_peptidase_M...	-5.77	1.86e-03	0.037000
k141_441355_16_Protein_of_unknown_function__DUF129		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_441355_16_Protein_of_un...	-5.76	2.51e-03	0.041000
k141_480101_1_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_1_-).pdf	-5.74	2.48e-03	0.041000
k141_116754_15_PFAM_binding-protein-dependent_tran		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116754_15_PFAM_bindin...	-5.73	1.61e-02	0.079600
k141_105059_11_Trypsin		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_11_Trypsin.pdf)	-5.72	1.04e-02	0.068900
k141_235579_24_Belongs_to_the_dihydroorotate_dehyd		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_24_Belongs_to_t_...	-5.71	1.07e-02	0.068900
k141_447245_50_Catalyzes_the_anaerobic_formation_o		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447245_50_Catalyzes_th...	-5.71	6.78e-03	0.056800
k141_480101_14_Pentapeptide		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_14_Pentapeptide...	-5.70	2.25e-02	0.093200
k141_91609_17_TIGRFAM_hopanoid_biosynthesis_associ		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_91609_17_TIGRFAM_hop...	-5.70	2.17e-03	0.039200
k141_321119_27_AIR_synthase_related_protein__N-ter		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_27_AIR_synthase...	-5.69	5.58e-03	0.055300
k141_302842_70_related_to_Ser_Thr_protein_kinases		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_302842_70_related_to_Se...	-5.65	9.63e-03	0.067100
k141_347826_3_lipoprotein_releasing_system__transm		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_347826_3_lipoprotein_rel...	-5.65	2.16e-02	0.092300
k141_55232_2_Arsenate_reductase_and_related		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_2_Arsenate_reduct...	-5.64	1.60e-02	0.079000
k141_151392_6_Catalyzes_the_interconversion_of_2-p		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_151392_6_Catalyzes_the...	-5.61	1.31e-02	0.073500
k141_116678_47_Protein_of_unknown_function__DUF350		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116678_47_Protein_of_un...	-5.60	2.93e-02	0.098700
k141_251933_47_Belongs_to_the_aspartokinase_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_251933_47_Belongs_to_t_...	-5.60	1.06e-02	0.068900
k141_137401_8_Histidine_kinase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_8_Histidine_kinas...	-5.58	5.89e-03	0.055800
k141_27722_7_Part_of_the_ABC_transporter_complex_M		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_27722_7_Part_of_the_AB...	-5.58	2.48e-02	0.095300
k141_288091_15_PFAM_FAD_dependent_oxidoreductase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_288091_15_PFAM_FAD_...	-5.58	2.01e-02	0.089100
k141_480234_60_BON_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_60_BON_domain...	-5.56	5.00e-03	0.055300
k141_318301_51_Cytochrome_C_oxidase__cbb3-type_su		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_51_Cytochrome_...	-5.54	1.98e-02	0.088900
k141_55541_30_A_type_II_topoisomerase_that_negativ		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_30_A_type_II_topo...	-5.54	1.17e-04	0.022500
k141_422130_15_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_422130_15_-).pdf	-5.52	1.37e-02	0.074500
k141_105059_65_Cell_wall_formation__Catalyzes_the		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_65_Cell_wall_for...	-5.51	1.15e-02	0.070400
k141_235579_12_Is_probably_a_protein_kinase_regula		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_12_Is_probably_...	-5.50	2.15e-02	0.092200
k141_105059_53_Thiamine_monophosphate_synthase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_53_Thiamine_mo...	-5.49	1.08e-02	0.068900
k141_105059_55_Part_of_the_Sec_protein_translocase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_55_Part_of_the_...	-5.48	3.55e-03	0.048400
k141_110203_2_Belongs_to_the_class-II_aminocycl-IR		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_110203_2_Belongs_to_th...	-5.48	1.37e-02	0.074500
k141_121273_5_Phospholipase_Carboxylesterase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_121273_5_Phospholipase...	-5.48	3.49e-03	0.048400
k141_173944_23_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_173944_23_-).pdf	-5.47	3.23e-04	0.026100
k141_400150_4_Citrate_transporter		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_400150_4_Citrate_transp...	-5.46	2.53e-02	0.095500
k141_11890_1_Integrase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_11890_1_Integrase.pdf)	-5.44	2.24e-02	0.093200
k141_321119_15_Part_of_the_outer_membrane_protein__		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_15_Part_of_the_o_...	-5.44	2.36e-02	0.094000
k141_29030_6_Specifically_methylates_the_50S_ribos		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_29030_6_Specifically_met...	-5.43	2.52e-02	0.095500
k141_29030_5_ABC-type_oligopeptide_transport_syste		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_29030_5_ABC-type_oligo...	-5.42	2.77e-02	0.098100
k141_447245_15_RF-1_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447245_15_RF-1_domain...	-5.42	1.07e-02	0.068900
k141_198809_10_RNaseP_catalyzes_the_removal_of_the		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198809_10_RNaseP_cata...	-5.41	7.16e-04	0.032300

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_55541_3_Murein-degrading_enzyme_that_degrades		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_3_Murein-degradin...	-5.41	7.71e-03	0.059100
k141_300744_9_Nucleotidase_that_shows_phosphatase_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_300744_9_Nucleotidase_t...	-5.40	5.43e-03	0.055300
k141_486098_14_TIGRFAM_ATP-dependent_helicase_HrpA		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486098_14_TIGRFAM_AT...	-5.40	2.15e-02	0.092200
k141_239940_4_May_be_involved_in_the_biosynthesis_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_239940_4_May_be_involv...	-5.39	2.97e-02	0.099200
k141_105059_54_Catalyzes_two_activities_which_are_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_54_Catalyzes_tw...	-5.38	4.89e-03	0.055300
k141_155751_16_Gliding_motility_protein_GldG		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_155751_16_Gliding_motili...	-5.38	2.54e-02	0.095500
k141_105059_42_PGAP1-like_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_42_PGAP1-like_...	-5.37	2.78e-02	0.098100
k141_294638_13_dna-binding_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_294638_13_dna-binding_...	-5.37	8.61e-03	0.063200
k141_92968_3_50S_ribosomal_protein_L31		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_3_50S_ribosomal_...	-5.37	2.07e-02	0.091100
k141_480101_23_ABC_transporter_urea		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_23_ABC_transpo...	-5.36	1.93e-02	0.088400
k141_153721_9_involved_in_the_biosynthesis_of_the_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_153721_9_involved_in_th...	-5.35	3.01e-02	0.099400
k141_411118_43_subfamily_IA_variant_1		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_411118_43_subfamily_IA_...	-5.34	6.50e-04	0.032300
k141_457880_22_cold-shock_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_457880_22_cold-shock_pr...	-5.34	1.18e-03	0.033000
k141_105059_69_involved_in_cell_wall_formation__Ca		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_69_involved_in_c...	-5.31	2.35e-02	0.094000
k141_226820_36_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_226820_36_-pdf)	-5.31	2.57e-02	0.095700
k141_354519_9_Catalyzes_the_conversion_of_D-ribulo		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_354519_9_Catalyzes_the_...	-5.31	2.19e-02	0.092400
k141_447245_46_small_GTP-binding_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447245_46_small_GTP-bi...	-5.31	3.33e-04	0.026100
k141_480101_4_Belongs_to_the_peptidase_S33_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_4_Belongs_to_th...	-5.30	2.60e-02	0.095800
k141_55541_17_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_17_-pdf)	-5.29	2.82e-02	0.098100
k141_457956_12_ABC-2_type_transporter		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_457956_12_ABC-2_type_t...	-5.27	1.80e-02	0.084600
k141_92968_34_Part_of_a_membrane_complex_involved_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_34_Part_of_a_me...	-5.27	2.24e-02	0.093200
k141_480101_22_Branched-chain_amino_acid_transport		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_22_Branched-cha...	-5.25	2.87e-02	0.098100
k141_105059_68_First_step_of_the_lipid_cycle_react		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_68_First_step_of_...	-5.24	3.03e-02	0.099400
k141_486291_13_Required_for_the_export_of_heme_to_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_13_Required_for_...	-5.23	2.19e-02	0.092400
k141_137401_31_Uncharacterised_signal_transduction		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_31_Uncharacteris...	-5.21	2.52e-02	0.095500
k141_15476_34_Outer_Membrane_Lipoprotein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_34_Outer_Membra...	-5.21	2.91e-02	0.098500
k141_299557_54_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_299557_54_-pdf)	-5.21	1.18e-02	0.071000
k141_435897_1_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_435897_1_-pdf)	-5.21	3.59e-05	0.012700
k141_116754_3_Pyrophosphatase_that_catalyzes_the_h		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116754_3_Pyrophosphata...	-5.20	2.22e-02	0.093000
k141_486291_47_PFAM_methyltransferase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_47_PFAM_methyl...	-5.19	8.25e-03	0.062000
k141_143192_36_Part_of_the_outer_membrane_protein_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_36_Part_of_the_...	-5.18	2.14e-02	0.092200
k141_251933_27_4Fe-4S_dicluster_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_251933_27_4Fe-4S_diclu...	-5.18	9.68e-04	0.032300
k141_116678_38_Protein_of_unknown_function__DUF101		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116678_38_Protein_of_un...	-5.17	9.55e-03	0.067000
k141_299557_43_type_I_secretion_outer_membrane_pro		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_299557_43_type_I_secreti...	-5.17	1.69e-02	0.081000
k141_15043_13_PFAM_Type_II_secretion_system_protei		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15043_13_PFAM_Type_II...	-5.16	6.03e-03	0.055900
k141_114613_2_TIGRFAM_CRISPR-associated_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_114613_2_TIGRFAM_CRI...	-5.13	1.16e-02	0.070500
k141_354519_3_Circularly_permuted_ATP-grasp_type_2		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_354519_3_Circularly_per...	-5.13	2.44e-02	0.095100

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_486291_50_PFAM_Citrate_transporter		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_50_PFAM_Citrate...)	-5.13	1.96e-02	0.088600
k141_196338_23_Rhodanese_Homology_Domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_196338_23_Rhodanese_...)	-5.11	1.52e-02	0.077400
k141_318301_52_it_can_initiate_unwinding_at_a_nick		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_52_it_can_initiate...)	-5.11	1.09e-02	0.068900
k141_288091_14_Catalyzes_the_conversion_of_1-hydro		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_288091_14_Catalyzes_th...)	-5.10	1.59e-02	0.079000
k141_35613_2_PFAM_transposase__IS4		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_35613_2_PFAM_transpos...)	-5.10	3.29e-05	0.012700
k141_288091_5_PFAM_FAD-dependent_pyridine_nucleoti		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_288091_5_PFAM_FAD-de...)	-5.07	1.07e-02	0.068900
k141_234601_29_CBS_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_29_CBS_domain...)	-5.04	2.00e-02	0.089100
k141_318301_53_COG1235_Metal-dependent_hydrolases_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_53_COG1235_M...)	-5.04	1.68e-02	0.081000
k141_235579_8_this_subunit_has_chaperone_activity_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_8_this_subunit_h...)	-5.02	2.68e-03	0.041000
k141_26457_6_Pyridoxal_5'-phosphate__PLP_-binding_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_26457_6_Pyridoxal_5'-ph...)	-5.01	1.07e-02	0.068900
k141_137401_13_DsrE_DsrF_DsrH-like_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_13_DsrE_DsrF_D...)	-4.99	3.20e-04	0.026100
k141_234601_36_TIGRFAM_Tyrosine_recombinase_XerD		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_36_TIGRFAM_Ty...)	-4.99	1.33e-02	0.073700
k141_307998_1_Multidrug_MFS_transporter		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_307998_1_Multidrug_MFS...)	-4.99	1.01e-03	0.032300
k141_151392_3_COG0790_FOG_TPR_repeat__SEL1_subfami		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_151392_3_COG0790_FO...)	-4.98	3.03e-03	0.044500
k141_35613_4_Phage_integrase__N-terminal_SAM-like_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_35613_4_Phage_integras...)	-4.96	1.48e-03	0.034900
k141_480234_42_antipporter		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_42_antipporter.pdf)	-4.95	1.71e-02	0.081300
k141_26457_3_PFAM_Phosphoribulokinase_uridine_kina		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_26457_3_PFAM_Phospho...)	-4.94	2.81e-03	0.042100
k141_335000_14_transcriptional_regulatory_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_335000_14_transcriptional...)	-4.94	2.80e-02	0.098100
k141_402410_5_Belongs_to_the_resistance-nodulation		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_402410_5_Belongs_to_th...)	-4.94	1.25e-02	0.072400
k141_189812_5_Catalyzes_the_transfer_of_a_dimethyl		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_5_Catalyzes_the...)	-4.93	3.43e-03	0.048400
k141_142133_7_radical_SAM_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_142133_7_radical_SAM_p...)	-4.91	2.19e-02	0.092400
k141_143192_34_May_be_involved_in_recombinational_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_34_May_be_invol...)	-4.89	1.83e-02	0.085400
k141_390169_21_HAD-hydrolase-like		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_21_HAD-hydrolase...)	-4.88	2.31e-02	0.094000
k141_390169_32_COG2197_Response_regulator_containi		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_32_COG2197_R...)	-4.85	1.88e-02	0.087100
k141_15476_73_Involved_in_the_biosynthesis_of_the_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_73_Involved_in_th...)	-4.83	1.53e-02	0.077400
k141_173944_22_Methylates_the_class_1_translation_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_173944_22_Methylates_th...)	-4.83	4.90e-03	0.055300
k141_175012_7_Helicase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_175012_7_Helicase.pdf)	-4.82	1.77e-02	0.083500
k141_181027_13_it_plays_a_direct_role_in_the_trans		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_181027_13_it_plays_a_dir...)	-4.82	2.45e-03	0.041000
k141_441527_4_May_be_involved_in_recombination		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_441527_4_May_be_involv...)	-4.82	2.59e-02	0.095700
k141_15043_23_Type_II_and_III_secretion_system_pro		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15043_23_Type_II_and_III...)	-4.81	2.72e-02	0.098000
k141_445525_8_ABC_transporter_transmembrane_region		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_445525_8_ABC_transport...)	-4.79	2.51e-02	0.095500
k141_137401_2_Belongs_to_the_RtcB_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_2_Belongs_to_th...)	-4.78	2.81e-02	0.098100
k141_347933_11_One_of_the_essential_components_for		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_347933_11_One_of_the_...)	-4.77	1.89e-03	0.037000
k141_105059_74_Belongs_to_the_MraZ_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_74_Belongs_to_t...)	-4.76	5.49e-03	0.055300
k141_153721_4_Involved_in_the_restart_of_stalled_r		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_153721_4_Involved_in_th...)	-4.76	6.12e-03	0.056300
k141_15476_71_Protein_of_unknown_function__DUF1302		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_71_Protein_of_unk...)	-4.76	1.07e-02	0.068900
k141_321119_6_Part_of_the_MsrPQ_system_that_repair		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_6_Part_of_the_M...)	-4.74	2.87e-02	0.098100

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_153721_10_Bacterial_transferase_hexapeptide__		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_153721_10_Bacterial_tran...	-4.73	2.84e-02	0.098100
k141_167532_5_Urate_oxidase_N-terminal		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_167532_5_Urate_oxidase...	-4.73	6.25e-04	0.032300
k141_234601_23_Calcineurin-like_phosphoesterase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_23_Calcineurin-li...	-4.73	1.38e-02	0.074500
k141_363128_6_COG0714_MoxR-like_ATPases		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_363128_6_COG0714_Mo...	-4.73	2.90e-02	0.098100
k141_167532_23_Allows_the_formation_of_correctly_c		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_167532_23_Allows_the_fo...	-4.72	2.11e-02	0.091600
k141_251933_32_Pyridine_nucleotide-disulphide_oxid		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_251933_32_Pyridine_nucl...	-4.72	2.32e-02	0.094000
k141_487992_11_Catalyzes_the_transfer_of_a_two-car		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_487992_11_Catalyzes_th...	-4.72	2.57e-04	0.026000
k141_137401_21_PFAM_Positive_regulator_of_sigma_E_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_21_PFAM_Positiv...	-4.71	2.87e-02	0.098100
k141_137401_69_PilZ_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_69_PilZ_domain...	-4.71	3.07e-02	0.099800
k141_55232_19_Catalyzes_the_formation_of_N_7_-meth		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_19_Catalyzes_the...	-4.71	4.16e-03	0.052600
k141_487992_12_PFAM_alkyl_hydroperoxide_reductase_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_487992_12_PFAM_alkyl_...	-4.69	6.23e-03	0.056600
k141_92968_28_COG1013_Pyruvate_ferredoxin_oxidored		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_28_COG1013_Pyr...	-4.69	1.71e-03	0.036300
k141_234601_8_Required_for_chromosome_condensation		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_8_Required_for_...	-4.67	8.31e-03	0.062000
k141_116678_52_Converts_GTP_to_7_8-dihydroneopteri		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116678_52_Converts_GT...	-4.63	3.33e-04	0.026100
k141_179467_21_-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_179467_21_-pdf)	-4.63	2.60e-02	0.095800
k141_486291_46_COG0741_Soluble_lytic_murein_transg		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_46_COG0741_S...	-4.63	1.94e-02	0.088400
k141_321119_10_Histone_deacetylase_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_10_Histone_deac...	-4.62	5.40e-03	0.055300
k141_390169_10_Phage_integrase_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_10_Phage_integr...	-4.62	3.03e-02	0.099400
k141_3035_52_Converts_o-succinylbenzoyl-CoA_OSB-C		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_3035_52_Converts_o-suc...	-4.61	2.67e-02	0.097500
k141_390169_30_Belongs_to_the_CDP-alcohol_phosphat		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_30_Belongs_to_t...	-4.59	2.29e-02	0.094000
k141_234601_39_PFAM_Thioredoxin		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_39_PFAM_Thiore...	-4.56	4.98e-03	0.055300
k141_480234_54_Component_of_the_ubiquinol-cytochro		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_54_Component_...	-4.56	1.30e-02	0.073500
k141_137401_12_Belongs_to_the_sulfur_carrier_prote		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_12_Belongs_to_t...	-4.55	1.02e-03	0.032300
k141_435897_4_Histidine_kinase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_435897_4_Histidine_kinas...	-4.55	2.44e-02	0.095100
k141_234601_28_Binds_the_second_messenger_bis-3'-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_28_Binds_the_se...	-4.54	7.37e-03	0.057500
k141_28580_9_Transcriptional_regulator_containing_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_28580_9_Transcriptional_...	-4.53	8.99e-04	0.032300
k141_318301_49_COG2863_Cytochrome_c553		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_49_COG2863_C...	-4.51	2.04e-03	0.038100
k141_55541_32_Belongs_to_the_D-isomer_specific_2-h		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_32_Belongs_to_th...	-4.51	1.40e-02	0.074800
k141_197578_6_Belongs_to_the_Dsrf_TusC_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_197578_6_Belongs_to_th...	-4.50	4.61e-03	0.054600
k141_445026_11_Alpha_amylase_catalytic_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_445026_11_Alpha_amylas...	-4.50	4.37e-03	0.052700
k141_354519_11_Converts_2_5-diamino-6--_ribosylamin		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_354519_11_Converts_2_5...	-4.48	1.07e-02	0.068900
k141_390169_34_ATPases_associated_with_a_variety_o		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_34_ATPases_ass...	-4.47	2.84e-02	0.098100
k141_101903_8_Protein_of_unknown_function__DUF3108		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_101903_8_Protein_of_unk...	-4.46	2.17e-02	0.092400
k141_235579_9_protein_conserved_in_bacteria		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_9_protein_conser...	-4.46	1.68e-02	0.081000
k141_189812_17_low_molecular_weight		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_17_low_molecula...	-4.44	1.03e-02	0.068900
k141_197578_5_TIGRFAM_sulfur_relay_protein_TusD_Ds		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_197578_5_TIGRFAM_sulf...	-4.44	1.53e-02	0.077400
k141_226820_28_Functions_as_both_a_chaperone_and_a		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_226820_28_Functions_as...	-4.44	7.39e-03	0.057500

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_105059_45_Adenosine-5'-phosphosulfate_reducta		-4.43	6.17e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_45_Adenosine-5'...
k141_143192_21_Involved_in_the_gluconeogenesis__Ca		-4.43	8.24e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_21_Involved_in_t...
k141_480101_7_1_-5-phosphoribosyl_-5_-phosphori		-4.43	5.57e-03	0.055300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480101_7_1_-5-phosphori...
k141_486291_33_-		-4.43	2.23e-02	0.093200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_33_- pdf)
k141_91609_5_PFAM_Cytochrome_bd_ubiquinol_oxidase_		-4.42	2.48e-02	0.095300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_91609_5_PFAM_Cytochro...
k141_333490_6_FAD_dependent_oxidoreductase		-4.41	4.43e-04	0.031200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_333490_6_FAD_depende...
k141_189812_6_This_protein_is_involved_in_the_repa		-4.35	2.65e-03	0.041000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_6_This_protein_is...
k141_422130_7_Stereospecific_condensation_of_phosp		-4.35	1.23e-02	0.072100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_422130_7_Stereospecific...
k141_55541_31_Catalyzes_the_reversible_conversion_		-4.35	5.74e-03	0.055300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_31_Catalyzes_the...
k141_183936_9_Catalyzes_the_reversible_conversion_		-4.33	2.55e-03	0.041000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183936_9_Catalyzes_the...
k141_189812_41_3'-5'_exoribonuclease_that_releases		-4.33	9.73e-03	0.067300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_41_3'-5'_exoribon...
k141_358336_15_Protein_of_unknown_function__DUF153		-4.33	7.43e-03	0.057500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_358336_15_Protein_of_un...
k141_480234_53_Component_of_the_ubiquinol-cytochro		-4.33	2.35e-02	0.094000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_53_Component_...
k141_134750_14_oxidoreductase_activity		-4.32	1.03e-02	0.068900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_134750_14_oxidoreductas...
k141_189812_33__GGDEF__domain		-4.31	7.12e-03	0.056800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_33__GGDEF__d...
k141_26457_10_Transfers_a_succinyl_group_from_succ		-4.28	1.48e-02	0.076200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_26457_10_Transfers_a_s...
k141_15476_22_Belongs_to_the_FAD-dependent_oxidore		-4.26	2.74e-03	0.041500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_22_Belongs_to_th...
k141_251933_26_Tetratricopeptide_repeat		-4.25	3.85e-03	0.050200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_251933_26_Tetratricopept...
k141_143192_20_PFAM_Preprotein_translocase_SecG_su		-4.24	1.77e-04	0.022700	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_20_PFAM_Prepr...
k141_143192_28_Belongs_to_the_CarA_family		-4.24	1.22e-02	0.072000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_28_Belongs_to_t...
k141_389277_22_Catalyzes_the_ferrous_insertion_int		-4.24	1.23e-02	0.072100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_389277_22_Catalyzes_th...
k141_251933_38_Catalyzes_the_formation_of_L-homocy		-4.22	1.99e-02	0.089100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_251933_38_Catalyzes_th...
k141_105059_48_Type_II_secretion_system		-4.20	3.29e-03	0.047800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_48_Type_II_secr...
k141_15476_2_Catalyzes_the_conversion_of_dihydroor		-4.19	2.46e-02	0.095100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_2_Catalyzes_the_...
k141_189812_16_Endoribonuclease_that_plays_a_centr		-4.17	5.21e-03	0.055300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_16_Endoribonuc...
k141_480234_43_ABC_transporter		-4.17	1.14e-02	0.070300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_43_ABC_transpo...
k141_226820_31_-		-4.16	2.93e-02	0.098700	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_226820_31_- pdf)
k141_457880_21_Belongs_to_the_DEAD_box_helicase_fa		-4.15	3.53e-03	0.048400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_457880_21_Belongs_to_t...
k141_197578_7_sulfur_relay_protein_TusB_DsrH		-4.12	3.07e-02	0.099800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_197578_7_sulfur_relay_pr...
k141_15476_62_electron_transfer_flavoprotein_beta_		-4.11	2.03e-02	0.089500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_62_electron_transf...
k141_179467_20_response_regulator_receiver		-4.11	3.00e-02	0.099400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_179467_20_response_reg...
k141_235579_15_TIGRFAM_DJ-1_family_protein		-4.11	8.30e-03	0.062000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_15_TIGRFAM_DJ...
k141_55232_18_PFAM_Fatty_acid_desaturase		-4.10	9.57e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_18_PFAM_Fatty_a...
k141_457880_19_-		-4.09	1.48e-02	0.076200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_457880_19_- pdf)
k141_55541_35_PFAM_Prephenate_dehydrogenase		-4.09	2.98e-02	0.099400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_35_PFAM_Prephe...
k141_116678_48_Cysteine-rich_domain		-4.07	3.03e-02	0.099400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116678_48_Cysteine-rich...
k141_234601_38_Required_for_disulfide_bond_formati		-4.06	1.36e-04	0.022500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_38_Required_for...

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_299557_46_Catalyzes_the_ADP_transfer_from_ATP		-4.06	4.28e-03	0.052700	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_299557_46_Catalyzes_th...
k141_294638_9_Protein_of_unknown_function__DUF255		-4.05	1.59e-02	0.079000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_294638_9_Protein_of_unk...
k141_457956_9_COG1051_ADP-ribose_pyrophosphatase		-4.05	2.09e-02	0.091200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_457956_9_COG1051_AD...
k141_234601_31_Involved_in_targeting_and_insertion		-4.03	8.17e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_31_Involved_in_t...
k141_173944_16_Involved_in_the_biosynthesis_of_the		-4.02	2.42e-02	0.095100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_173944_16_Involved_in_t...
k141_105059_17_Adds_poly_A_tail_to_the_3'_end_of_		-4.01	8.02e-03	0.060800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_17_Adds_poly_A...
k141_155751_8_Involved_in_the_biosynthesis_of_bran		-4.01	9.84e-03	0.067300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_155751_8_Involved_in_th...
k141_179467_4_Catalyzes_the_attachment_of_threonin		-4.01	1.88e-03	0.037000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_179467_4_Catalyzes_the...
k141_15043_10_PFAM_transposase_JS111A_JS1328_JS153		-3.97	1.46e-03	0.034900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15043_10_PFAM_transpo...
k141_208287_1_Putative_transposase		-3.95	2.38e-02	0.094500	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_208287_1_Putative_trans...
k141_73063_7_Belongs_to_the_argininosuccinate_synt		-3.95	1.43e-02	0.076000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_73063_7_Belongs_to_the...
k141_26457_16_Catalyzes_the_transfer_of_a_ribosyl_		-3.91	1.01e-02	0.068900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_26457_16_Catalyzes_the...
k141_35613_3_Putative_transposase		-3.91	1.20e-03	0.033000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_35613_3_Putative_transp...
k141_486291_15_once_thought_to_export_heme_this_s		-3.91	3.07e-02	0.099800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_15_once_thought...
k141_288091_10_-		-3.90	2.87e-02	0.098100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_288091_10_-pdf)
k141_347933_12_Participates_in_both_transcription_		-3.90	2.33e-02	0.094000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_347933_12_Participates_i...
k141_3035_8_Catalyzes_the_condensation_of__S_-aspa		-3.88	3.44e-03	0.048400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_3035_8_Catalyzes_the_c...
k141_335000_13_Nuclease_that_resolves_Holliday_jun		-3.88	2.82e-02	0.098100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_335000_13_Nuclease_tha...
k141_400150_6_-		-3.88	6.63e-04	0.032300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_400150_6_-pdf)
k141_55232_20_Catalyzes_the_rearrangement_of_1-deo		-3.88	1.41e-03	0.034900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_20_Catalyzes_the...
k141_15476_66_dehydrogenase_domain_of_multifunctio		-3.86	1.66e-02	0.081000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_66_dehydrogenas...
k141_317927_2_PFAM_peptidase		-3.84	1.95e-02	0.088400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_317927_2_PFAM_peptida...
k141_167532_25_Allows_the_formation_of_correctly_c		-3.82	3.07e-02	0.099800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_167532_25_Allows_the_fo...
k141_3035_37_polysaccharide_export_protein		-3.82	3.68e-03	0.048900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_3035_37_polysaccharide_...
k141_480234_68_Transposase_zinc-ribbon_domain		-3.81	9.55e-03	0.067000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_68_Transposase...
k141_198809_14_A_type_II_topoisomerase_that_negati		-3.80	1.72e-03	0.036300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198809_14_A_type_II_top...
k141_358250_2_PFAM_Aminotransferase_class_I_and_II		-3.80	5.20e-03	0.055300	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_358250_2_PFAM_Aminotr...
k141_447245_36_Belongs_to_the_B11_family		-3.79	2.36e-04	0.026000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447245_36_Belongs_to_t...
k141_480234_40_Involved_in_the_biosynthesis_of_lip		-3.78	2.76e-02	0.098100	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_40_Involved_in_t...
k141_358336_10_Protein_of_unknown_function__DUF284		-3.76	1.89e-02	0.087200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_358336_10_Protein_of_un...
k141_302180_10_Methyl-accepting_chemotaxis-like_do		-3.75	3.09e-02	0.100000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_302180_10_Methyl-accept...
k141_441088_3_PFAM_Major_Facilitator_Superfamily		-3.75	1.69e-02	0.081000	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_441088_3_PFAM_Major_...
k141_480234_10_Belongs_to_the_Smg_family		-3.75	1.07e-02	0.068900	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_10_Belongs_to_t...
k141_208287_2_Putative_transposase		-3.74	3.03e-02	0.099400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_208287_2_Putative_trans...
k141_302027_3_Component_of_the_pyruvate_dehydrogen		-3.72	1.52e-02	0.077400	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_302027_3_Component_of_...
k141_55541_38_thus_facilitating_recognition_of_the		-3.72	6.45e-03	0.056800	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55541_38_thus_facilitatn...
k141_234601_19_protein_histidine_kinase_activity		-3.71	4.70e-03	0.055200	(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_19_protein_histidi...

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_457880_14_EamA-like_transporter_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_457880_14_EamA-like_tr...	-3.71	2.97e-02	0.099200
k141_333490_8_4Fe-4S_dicuster_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_333490_8_4Fe-4S_diclust...	-3.70	9.46e-03	0.067000
k141_73063_14_COG0745_Response_regulators_consisti		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_73063_14_COG0745_Re...	-3.70	9.47e-04	0.032300
k141_183573_21_Transcription_factor_that_acts_by_b		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183573_21_Transcription...	-3.68	5.26e-03	0.055300
k141_189812_30_aminotransferase_class_I_and_II		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_30_aminotransfer...	-3.68	3.96e-03	0.050700
k141_491901_8_Malate_synthase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_491901_8_Malate_syntha...	-3.68	8.67e-04	0.032300
k141_134750_13_Peptidase_M16		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_134750_13_Peptidase_...	-3.67	8.57e-03	0.063200
k141_134750_5_Transglutaminase-like_superfamily		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_134750_5_Transglutamin...	-3.67	6.15e-03	0.056300
k141_137401_23_Required_for_accurate_and_efficient		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_23_Required_for...	-3.67	1.24e-02	0.072200
k141_181027_12_ATP_synthase_I_chain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_181027_12_ATP_synthas...	-3.67	8.04e-04	0.032300
k141_32866_5_Nitrilase_cyanide_hydratase_and_apoli		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_32866_5_Nitrilase_cyanid...	-3.67	1.17e-02	0.070700
k141_189812_12_Cytochrome_c		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_12_Cytochrome_...	-3.66	2.36e-02	0.094000
k141_294638_11_Belongs_to_the_UPF0276_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_294638_11_Belongs_to_t...	-3.66	2.69e-02	0.097800
k141_143192_30_ATP_binding_to_DnaK_triggers_the_re		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_30_ATP_binding_...	-3.65	2.87e-02	0.098100
k141_15476_10_COG1278_Cold_shock_proteins		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_10_COG1278_Col...	-3.65	2.07e-03	0.038100
k141_6600_18_Cytochrome_c		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_6600_18_Cytochrome_c_p...	-3.65	2.83e-02	0.098100
k141_134750_18_Transposase_IS66_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_134750_18_Transposase...	-3.64	2.55e-02	0.095500
k141_197578_11_PFAM_FAD-dependent_pyridine_nucleot		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_197578_11_PFAM_FAD-d...	-3.63	3.90e-03	0.050400
k141_321119_7_Part_of_the_MsrPQ_system_that_repair		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_7_Part_of_the_M...	-3.63	1.40e-03	0.034900
k141_486291_59_peptidylprolyl_isomerase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_59_peptidylprolyl...	-3.63	1.47e-02	0.076200
k141_181027_22_Catalyzes_the_last_two_sequential_r		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_181027_22_Catalyzes_th...	-3.61	6.92e-03	0.056800
k141_480234_18_TIGRFAM_Amino_acid_adenylation		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_18_TIGRFAM_A...	-3.61	3.61e-03	0.048400
k141_116754_8_In_eubacteria_ppGpp_guanosine_3'-di		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116754_8_In_eubacteria_...	-3.60	7.58e-03	0.058400
k141_155751_22_Belongs_to_the_HesB_IscA_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_155751_22_Belongs_to_t...	-3.59	2.62e-03	0.041000
k141_55232_36_glutamate--cysteine_ligase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_36_glutamate--cys...	-3.59	6.70e-03	0.056800
k141_158408_18_Cytochrome_c554_and_c-prime		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_158408_18_Cytochrome_...	-3.58	8.65e-03	0.063200
k141_402762_1_Facilitates_transcription_terminatio		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_402762_1_Facilitates_tran...	-3.58	3.59e-03	0.048400
k141_92968_31_Oxidoreductase_required_for_the_tran		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_31_Oxidoreductas...	-3.58	4.87e-04	0.032300
k141_189812_39_Binds_together_with_S18_to_16S_ribo		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_39_Binds_togeth...	-3.57	2.45e-02	0.095100
k141_260350_8_Belongs_to_the_resistance-nodulation		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_260350_8_Belongs_to_th...	-3.56	4.95e-03	0.055300
k141_447245_20_Sigma_factors_are_initiation_factor		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447245_20_Sigma_factor...	-3.55	2.65e-03	0.041000
k141_486291_32_Protein_of_unknown_function_DUF283		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_32_Protein_of_un...	-3.55	2.19e-02	0.092400
k141_235579_7_Protease_subunit_of_a_proteasome-lik		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_7_Protease_subu...	-3.54	1.95e-02	0.088400
k141_328637_1_Belongs_to_the_CinA_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_328637_1_Belongs_to_th...	-3.53	6.28e-03	0.056800
k141_389277_20_Transcriptional_regulator		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_389277_20_Transcription...	-3.53	9.94e-04	0.032300
k141_389277_24_Catalyzes_the_reversible_transfer_o		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_389277_24_Catalyzes_th...	-3.53	2.37e-02	0.094000
k141_92968_22_Catalyzes_the_decarboxylation_of_fou		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_22_Catalyzes_the...	-3.53	7.03e-03	0.056800

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			p- Value	Adjusted p-Value	
k141_411118_38_Catalyzes_the_deamination_of_5-meth		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_411118_38_Catalyzes_the...	-3.52	2.57e-02	0.095700
k141_427592_4_Interacts_with_and_stabilizes_bases_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_427592_4_Interacts_with...	-3.52	5.96e-03	0.055900
k141_32866_17_NapD_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_32866_17_NapD_protein...	-3.51	1.60e-02	0.079000
k141_189812_11_3'-to-5'-exoribonuclease_specific_f		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_11_3'-to-5'-exorib...	-3.49	1.44e-02	0.076000
k141_183573_3_SMART_Adenylyl_cyclase_class-3_4_gua		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183573_3_SMART_Aden...	-3.46	2.81e-02	0.098100
k141_355308_4_Belongs_to_the_class-II_pyridine_nuc		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_355308_4_Belongs_to_th...	-3.45	5.77e-03	0.055300
k141_318301_47_Necessary_for_normal_cell_division_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_47_Necessary_fo...	-3.43	1.65e-02	0.081000
k141_198283_1_iron_dependent_repressor		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198283_1_iron_depend...	-3.42	9.67e-03	0.067100
k141_300744_2_Catalyzes_the_ATP-dependent_aminatio		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_300744_2_Catalyzes_the...	-3.42	7.22e-03	0.057200
k141_313594_2_Belongs_to_the_anaerobic_coproporph		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_313594_2_Belongs_to_th...	-3.41	7.09e-03	0.056800
k141_363128_8_Catalyzes_the_acyloin_condensation_r		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_363128_8_Catalyzes_the...	-3.41	2.10e-02	0.091200
k141_189812_3_GTPase_that_associates_with_the_50S_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_189812_3_GTPase_that...	-3.40	2.86e-03	0.042400
k141_3035_43_Belongs_to_the_prokaryotic_molybdopte		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_3035_43_Belongs_to_the...	-3.39	2.89e-02	0.098100
k141_116756_7_AIR_synthase_related_protein_N-term		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116756_7_AIR_synthase...	-3.37	8.61e-03	0.063200
k141_480234_48_Cell_wall_formation_Adds_enolpyruv		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_48_Cell_wall_for...	-3.37	1.54e-02	0.077700
k141_486291_64_Involved_in_protein_export_Acts_as		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_64_Involved_in_p...	-3.36	7.04e-03	0.056800
k141_137401_65_PFAM_4Fe-4S_ferredoxin_iron-sulfur_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_65_PFAM_4Fe-4...	-3.35	3.09e-02	0.100000
k141_288091_1_Iron-sulfur_cluster_insertion_prot		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_288091_1_Iron-sulfur_clu...	-3.35	2.51e-02	0.095500
k141_197578_3_reductase_dissimilatory-type_alpha_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_197578_3_reductase_dis...	-3.34	6.00e-03	0.055900
k141_143192_22_Catalyzes_the_conversion_of_glucosa		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_22_Catalyzes_th...	-3.33	2.35e-02	0.094000
k141_354519_13_Catalyzes_the_reversible_interconve		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_354519_13_Catalyzes_th...	-3.33	1.17e-02	0.070700
k141_480234_11_Releases_the_supercoiling_and_torsi		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_11_Releases_the...	-3.33	1.22e-02	0.072000
k141_183573_9_Provides_the_precursors_necessary_fo		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_183573_9_Provides_the_...	-3.31	2.56e-02	0.095700
k141_321119_13_Myo-inositol-1-phosphate_synthase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_13_Myo-inositol-1...	-3.31	2.68e-02	0.097500
k141_370813_30_ATPase_that_binds_to_both_the_70S_r		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_370813_30_ATPase_that...	-3.31	2.14e-02	0.092200
k141_318301_3_Belongs_to_the_GARS_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_3_Belongs_to_th...	-3.30	2.54e-02	0.095500
k141_101903_10_Binds_and_transfers_iron-sulfur_Fe		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_101903_10_Binds_and_tr...	-3.29	3.58e-03	0.048400
k141_134750_6_Belongs_to_the_PEP-utilizing_enzyme_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_134750_6_Belongs_to_th...	-3.29	1.88e-02	0.087100
k141_234601_32_Belongs_to_the_bacterial_ribosomal		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_32_Belongs_to_t...	-3.27	2.33e-02	0.094000
k141_143192_27_Belongs_to_the_CarB_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_27_Belongs_to_...	-3.26	1.31e-02	0.073600
k141_299557_40_Catalyzes_the_synthesis_of_the_hydr		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_299557_40_Catalyzes_th...	-3.26	6.36e-03	0.056800
k141_331758_4_Part_of_the_outer_membrane_protein_a		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_331758_4_Part_of_the_o...	-3.26	1.97e-02	0.088700
k141_491901_12_Catalyzes_the_phosphorylation_of_py		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_491901_12_Catalyzes_th...	-3.26	2.32e-03	0.040800
k141_55232_5_COG0526_Thiol-disulfide_isomerase_and		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_5_COG0526_Thiol...	-3.25	1.67e-02	0.081000
k141_23864_21_PFAM_PrkA_AAA		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_23864_21_PFAM_PrkA_A...	-3.24	1.90e-03	0.037000
k141_92968_27_Pyruvate_ferredoxin_oxidoreductase_a		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_92968_27_Pyruvate_ferre...	-3.21	1.60e-03	0.036300
k141_235579_16_Belongs_to_the_peptidase_S41A_famil		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_16_Belongs_to_t...	-3.20	5.65e-03	0.055300

ID	Image	logFC	From	From	From
			to	to	to
			p-Value	Adjusted p-Value	
k141_44285_10_NiFe_NiFeSe_hydrogenase_small_subuni		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_44285_10_NiFe_NiFeSe_...	-3.20	1.33e-02	0.073700
k141_381307_10_PFAM_Lytic_transglycosylase_catalyt		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_381307_10_PFAM_Lytic_t...	-3.19	2.66e-02	0.097500
k141_15476_72_Belongs_to_the_aldehyde_dehydrogenas		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_72_Belongs_to_th...	-3.18	4.93e-03	0.055300
k141_197578_4_reductase__dissimilatory-type_beta_s		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_197578_4_reductase_dis...	-3.16	6.59e-03	0.056800
k141_32866_6_Flavocytochrome_c_sulphide_dehydrogen		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_32866_6_Flavocytochrom...	-3.16	1.43e-02	0.076000
k141_143192_25_Specifically_methylates_the_uridine		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_25_Specifically_...	-3.15	1.69e-02	0.081000
k141_302842_54_Belongs_to_the_bacterial_ribosomal_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_302842_54_Belongs_to_t...	-3.15	1.35e-02	0.074400
k141_302842_55_Yqey-like_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_302842_55_Yqey-like_pro...	-3.11	2.25e-02	0.093200
k141_235579_18_regulatory_protein__arsR		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_235579_18_regulatory_pr...	-3.10	2.09e-02	0.091200
k141_318301_48_Cytochrome_c		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_48_Cytochrome_...	-3.09	1.94e-02	0.088400
k141_101903_25_belongs_to_the_aldehyde_dehydrogena		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_101903_25_belongs_to_t...	-3.08	1.38e-02	0.074500
k141_480234_6_Attaches_a_formyl_group_to_the_free_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_6_Attaches_a_for...	-3.07	2.97e-02	0.099200
k141_198918_9_TIGRFAM_glutamine_synthetase_type_I		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198918_9_TIGRFAM_glut...	-3.06	1.45e-02	0.076100
k141_32866_12_Seven_times_multi-haem_cytochrome_Cx		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_32866_12_Seven_times_...	-3.06	1.31e-02	0.073500
k141_402762_4_smart_pdz_dhr_glgf		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_402762_4_smart_pdz_dhr...	-3.04	2.29e-02	0.094000
k141_137401_18_Belongs_to_the_sigma-70_factor_fami		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_18_Belongs_to_t...	-3.02	2.27e-03	0.040600
k141_151392_9_PFAM_ErK_YbiS_YcFS_YnhG_family_prot		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_151392_9_PFAM_ErK_Y...	-3.01	8.91e-03	0.064300
k141_480234_7_Removes_the_formyl_group_from_the_N-		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_480234_7_Removes_the_...	-3.01	1.30e-02	0.073500
k141_27722_4_CoA-binding_domain		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_27722_4_CoA-binding_do...	-3.00	7.02e-03	0.056800
k141_105059_25_Presumably_involved_in_the_processi		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_25_Presumably_I...	-2.99	2.66e-02	0.097500
k141_347933_15_PFAM_Flagellar_hook-length_control_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_347933_15_PFAM_Flagell...	-2.98	1.85e-02	0.086100
k141_321119_18_Domain_of_unknown_function__DUF4115		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_321119_18_Domain_of_u...	-2.97	2.87e-02	0.098100
k141_151392_24_PFAM_Radical_SAM		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_151392_24_PFAM_Radic...	-2.96	1.36e-02	0.074500
k141_234601_21_LTXXQ_motif_family_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_234601_21_LTXXQ_motif...	-2.94	6.70e-03	0.056800
k141_32866_16_Molybdopterin_oxidoreductase_Fe4S4_d		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_32866_16_Molybdopterin...	-2.93	1.29e-02	0.073500
k141_486291_62_ATP-dependent_specificity_component		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_62_ATP-depende...	-2.92	1.56e-02	0.078200
k141_137401_22_Belongs_to_the_peptidase_S1C_family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_22_Belongs_to_t...	-2.91	1.12e-02	0.069600
k141_73063_6_Diguanylate_cyclase		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_73063_6_Diguanylate_cyc...	-2.90	2.33e-02	0.094000
k141_55232_32_Belongs_to_the_UPF0301__AlgH__family		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_55232_32_Belongs_to_th...	-2.89	2.46e-02	0.095100
k141_116754_5_PFAM_YicC-like		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_116754_5_PFAM_YicC-lik...	-2.87	1.45e-02	0.076100
k141_335000_50_Belongs_to_the_mannose-6-phosphate_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_335000_50_Belongs_to_t...	-2.85	1.15e-02	0.070300
k141_101903_20_protein_conserved_in_bacteria		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_101903_20_protein_cons...	-2.83	1.21e-02	0.072000
k141_143192_31_Heat_shock_70_kDa_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_31_Heat_shock_...	-2.82	1.70e-02	0.081000
k141_137401_71_The_UvrABC_repair_system_catalyzes_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_71_The_UvrABC...	-2.78	2.71e-02	0.098000
k141_143192_33_Negative_regulator_of_class_I_heat_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_143192_33_Negative_reg...	-2.77	1.39e-02	0.074700
k141_151392_19_FeS_assembly_SUF_system_protein_Suf		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_151392_19_FeS_assembl...	-2.77	5.80e-03	0.055300
k141_105059_44_reductase__alpha_subunit		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_105059_44_reductase__a...	-2.76	1.39e-02	0.074700

ID	Image	logFC	From to	From to	From to
			p- Value	Adjusted p-Value	
k141_137401_19_PFAM_Anti_sigma-E_protein_RseA		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_137401_19_PFAM_Anti_s...	-2.72	5.80e-03	0.055300
k141_486291_63_Cleaves_peptides_in_various_protein		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_63_Cleaves_pept...	-2.72	2.46e-02	0.095100
k141_44158_2_TIGRFAM_FeS_assembly_protein_SufB		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_44158_2_TIGRFAM_FeS...	-2.66	2.00e-02	0.089100
k141_15476_3_Oxidoreductase_required_for_the_trans		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_3_Oxidoreductase...	-2.59	1.25e-02	0.072300
k141_251933_44_Can_catalyze_the_hydrolysis_of_ATP_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_251933_44_Can_catalyze...	-2.59	1.77e-02	0.083500
k141_486291_10_Cytochrome_c-type_biogenesis_protei		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_486291_10_Cytochrome_...	-2.49	2.88e-02	0.098100
k141_155751_10_Thiamine_pyrophosphate_enzyme__N-te		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_155751_10_Thiamine_pyr...	-2.32	2.86e-02	0.098100
k141_318301_43_General__non_sugar-specific__compon		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_318301_43_General__no...	-2.25	2.44e-02	0.095100
k141_390169_20_AcnD-accessory_protein_PrpF		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_390169_20_AcnD-access...	-2.25	2.71e-02	0.098000
k141_447657_2_Transcriptional_regulator		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_447657_2_Transcriptional...	-2.22	1.04e-02	0.068900
k141_15476_5_General__non_sugar-specific__componen		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_15476_5_General__non_...	-2.09	1.48e-02	0.076200
k141_175746_1_transporter__dctM_subunit		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_175746_1_transporter__d...	1.76	2.50e-02	0.095500
k141_455273_1_TIGRFAM_formate_dehydrogenase__alpha		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_455273_1_TIGRFAM_for...	1.76	2.58e-02	0.095700
k141_198365_12_This_is_1_of_the_proteins_that_bind		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198365_12_This_is_1_of_...	1.86	2.81e-02	0.098100
k141_198365_11_One_of_the_proteins_that_surrounds_		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198365_11_One_of_the_...	1.88	3.00e-02	0.099400
k141_469349_1_Succinyl-CoA_synthetase_functions_in		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_469349_1_Succinyl-CoA_...	1.88	1.82e-02	0.085400
k141_245017_3_Ribosomal_protein_L19		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_245017_3_Ribosomal_pro...	1.93	2.78e-02	0.098100
k141_226857_1_Proton_pump_that_utilizes_the_energy		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_226857_1_Proton_pump_...	1.98	2.86e-02	0.098100
k141_370053_3_The_natural_substrate_for_this_enzym		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_370053_3_The_natural_s...	1.99	2.41e-02	0.095000
k141_483966_1_Protein_of_unknown_function__DUF3604		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_483966_1_Protein_of_unk...	2.07	2.86e-02	0.098100
k141_198365_17_Located_at_the_back_of_the_30S_subu		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198365_17_Located_at_t...	2.10	1.69e-02	0.081000
k141_416884_1_The_central_subunit_of_the_protein_t		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_416884_1_The_central_s...	2.15	1.53e-02	0.077400
k141_362726_2_Belongs_to_the_UDP-glucose_GDP-manno		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_362726_2_Belongs_to_th...	2.17	2.07e-02	0.091100
k141_166672_4_Proton-conducting_membrane_transport		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_166672_4_Proton-conduct...	2.20	1.35e-02	0.074400
k141_359974_3_phosphate-selective_porin_O_and_P		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_359974_3_phosphate-sel...	2.21	1.11e-02	0.069600
k141_198365_1_Forms_part_of_the_polypeptide_exit_t		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198365_1_Forms_part_of_...	2.27	9.33e-03	0.066400
k141_474591_1_Belongs_to_the_resistance-nodulation		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_474591_1_Belongs_to_th...	2.27	4.26e-03	0.052700
k141_198365_8_Belongs_to_the_universal_ribosomal_p		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198365_8_Belongs_to_th...	2.32	2.33e-02	0.094000
k141_148677_3_Belongs_to_the_membrane_fusion_prote		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_148677_3_Belongs_to_th...	2.37	9.16e-03	0.065600
k141_198365_16_This_is_one_of_the_proteins_that_bi		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_198365_16_This_is_one_...	2.76	7.13e-03	0.056800
k141_239481_1_Type_III_restriction_enzyme__res_sub		(figuresHS prok gamma RNAseq_analysis_with_DESeq2_longer_namesHvA/boxplot.k141_239481_1_Type_III_restri...	3.68	1.11e-03	0.032300

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